

38-21(52806) Sequence Listing_PCT_2.ST25.txt
SEQUENCE LISTING

<110> Monsanto Technology LLC

Baum, James A.
Donovan, Judith C.

Donovan, William P.

Engleman, James T.

Krasomil-Osterfeld, Karina

Pitkin, John W.

Roberts, James K.

<120> Insecticidal Proteins Secreted From Bacillus Species and Uses Therefor

<130> 38-21(52806)PCT

<150> US 60/485,483

<151> 2003-07-07

<160> 33

<170> PatentIn version 3.1

<210> 1

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<212> PRT

<213> Bacillus thuringiensis

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38-21(52806) Sequence Listing_PCT_2.ST25.txt

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Met Lys Asn Arg Phe Ser Lys
1 5gtg gca tta tgc acc gta ccg att tta atg gtt tct aca ttc gcc agt 221
Val Ala Leu Cys Thr Val Pro Ile Leu Met Val Ser Thr Phe Ala Ser
10 15 20tca agc atg tca gct ttt gct gca gaa gcc aaa tca cca gat tta aat 269
Ser Ser Met Ser Ala Phe Ala Ala Glu Ala Lys Ser Pro Asp Leu Asn
25 30 35gta tct caa caa gta ata ggt ccc tat gcc gaa tct tat att gat att 317
Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile
40 45 50 55gtg cag gat aga atg aaa caa agg gat aag gga tca aaa tta act ggt 365
Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly
60 65 70aaa cca ata aat atg caa gaa caa ata ata gat ggg tgg ttt cta gct 413
Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala
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38-21(52806) Sequence Listing_PCT_2.ST25.txt																
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Phe	Ile	Ser	Trp	Phe	Lys	Asp	Asn	Ile	Ala	Ser	Ser	Lys	Gly	Tyr	Asn	
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Ser	Ile	Ala	Glu	Gln	Met	Gly	Leu	Lys	Ile	Glu	Ala	Glu	Asn	Asp	Met	
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Asp	Val	Thr	Asn	Ile	Asp	Tyr	Thr	Ser	Lys	Thr	Gly	Asp	Thr	Ile	Tyr	
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Asn	Gly	Ile	Ser	Glu	Leu	Lys	Asn	Tyr	Thr	Gly	Ser	Thr	Gln	Lys	Met	
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		170					175					180				
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Pro	Ser	Gln	Glu	Val	Thr	Leu	Pro	Pro	Gly	His	Lys	Ala	Ile	Val	Lys	
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Tyr	Pro	Asn	Tyr	Arg	Glu	Ile	Asn	Leu	Ser	Asp	Ile	Arg	Glu	Thr	Met	
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Leu	Val	Gly	Val	Lys	Asn	His	Ile	Lys	Asn	Gly	Glu	Thr	Leu	Tyr	Ile	
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38-21(52806) Sequence Listing_PCT_2.ST25.txt

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gta tta agt gaa aac ttt aaa ttg 1253
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<212> PRT

<213> Bacillus thuringiensis

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 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
 50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
 100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
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Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr

38-21(52806) Sequence Listing_PCT_2.ST25.txt
 165 170 175

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 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
 225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu
 275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
 290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
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tttatatagg tttcatctaa ttttcaagac atgtgggtgt tttgcgtttt cttcttccaa      180
at ttgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact      240
gaaacatcac gatagcttaa agcaaaacga caatagtagc ggacggctac cataataata      300
tcttgtttga actgtttccc tttaaaatat cacatttgtg attctcctcg atgctttttt      360
tagagtgtag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa      420
accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaa catacgatgt      480
tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac      538
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                                     1

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Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr
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aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg      634
Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser
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cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct      682
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tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca      730
Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser
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aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga      778
Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly
70                                     75                                     80

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85                                     90                                     95

caa aca aat aga ttt ata tcc tgg ttt aaa gat aat ctt gct agt tcg      874
Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser
100                                     105                                     110                                     115

aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca      922
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120                                     125                                     130

tta aat gat atg gat gta aca aat att gat tat aca tct aaa aca ggt      970
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38-21(52806) Sequence Listing_PCT_2.ST25.txt
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Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser	
165 170 175	
gaa tcc act tca gta aca aat ggg tta caa tta gga ttt aaa gtt gct	1114
Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala	
180 185 190 195	
gct aag gga gta gtt gca tta gca ggt gca gat ttt gaa aca agt gtt	1162
Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val	
200 205 210	
acc tat aat tta tca tct act aca act gaa aca aat aca ata tcg gat	1210
Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp	
215 220 225	
aag ttt act gtt cca tct caa gaa gtt aca tta tcc cca gga cat aaa	1258
Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro Gly His Lys	
230 235 240	
gca gtg gtg aaa cat gat ttg aga aaa atg gtg tat ttt ggg act cat	1306
Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe Gly Thr His	
245 250 255	
gat tta aag ggt gat tta aaa gta ggt ttt aat gat aaa gag att gta	1354
Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys Glu Ile Val	
260 265 270 275	
caa aaa ttt att tat cca aat tat aga tca att gat tta tct gat att	1402
Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu Ser Asp Ile	
280 285 290	
cgt aaa aca atg att gaa att gat aaa tgg aat cat gta aat acc att	1450
Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val Asn Thr Ile	
295 300 305	
gac ttt tat caa tta gtt gga gtt aaa aat cat ata aaa aat ggt gat	1498
Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Asp	
310 315 320	
act tta tat ata gat acc ccg gcc gaa ttt aca ttt aat gga gct aat	1546
Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn Gly Ala Asn	
325 330 335	
cca tat tat aga gca aca ttt aca gaa tac gac gag aac gga aat cct	1594
Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Pro	
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38-21(52806) Sequence Listing_PCT_2.ST25.txt

<212> PRT

<213> Bacillus thuringiensis

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 35 40 45

Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp
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Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
 100 105 110

Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr
 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr
 210 215 220

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro
 225 230 235 240

Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys
 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu
 275 280 285

Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val
 290 295 300

Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn
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<213> Bacillus thuringiensis

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38-21(52806) Sequence Listing_PCT_2.ST25.txt

Met Lys Tyr
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Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Glu Thr Thr Leu	
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Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg Ala Glu Ser	
40 45 50	
tat att gat att gta caa gat aga atg aaa caa agg gat ata gaa tcg	369
Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp Ile Glu Ser	
55 60 65	
aaa cgt act ggt aaa ccg att aat atg caa gaa caa ata ata gat gga	417
Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly	
70 75 80	
tgg ttt tta gca aga ttc tgg ata ttt aaa gat caa aat aat aac cat	465
Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His	
85 90 95	
caa aca aat aga ttc ata aca tgg ttt aaa aat aat gtt gcc agc tca	513
Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val Ala Ser Ser	
100 105 110 115	
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Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ser	
120 125 130	
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Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly Lys Lys Gly	
135 140 145	
gat act ata tat aat ggc gtt tcg gaa tta gaa aat aaa atg gga aca	657
Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys Met Gly Thr	
150 155 160	
cct caa aaa atg aaa tca gat agt ttt caa aga gat tat acc aaa tct	705
Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser	
165 170 175	
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Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val Lys Val Ser	
180 185 190 195	
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Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu Thr Ser Val	
200 205 210	
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Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr Thr Ser Asp	
215 220 225	
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Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys	
230 235 240	

38-21(52806) Sequence Listing_PCT_2.ST25.txt

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caa aaa ttt att tat cca aat tat aga tct ata aat tta tct gat att Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu Ser Asp Ile 280 285 290	1041
cgt aaa aca atg aaa gaa att gat gaa tgg aat cat gta aaa ccc att Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val Lys Pro Ile 295 300 305	1089
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acc tta tat ata gag act cca gct aaa ttt att ttt aat gga gct aat Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn Gly Ala Asn 325 330 335	1185
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aatgtttttt tatgaggttt gtgtattcct atttgagcct ggaacggaac cattttgagt	1462
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38-21(52806) Sequence Listing_PCT_2.ST25.txt

Thr Thr Leu Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg
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 65 70 75 80
 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95
 Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val
 100 105 110
 Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125
 Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly
 130 135 140
 Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys
 145 150 155 160
 Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr
 165 170 175
 Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val
 180 185 190
 Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu
 195 200 205
 Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr
 210 215 220
 Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
 225 230 235 240
 Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser
 245 250 255
 Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys
 260 265 270
 Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu
 275 280 285

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val
 290 295 300

Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn
 325 330 335

Gly Ala Asn Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp
 340 345 350

Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu
 355 360 365

<210> 9

<211> 1378

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (215)..(1306)

<223>

<400> 9
 cagtggatag gaatttgttt tcgtgctagg tatcaattta atttgttcta taagataagt 60
 gaagtacgat caaaatgaat acttttgtgt attagatcaa taggtaaaat aataataaat 120
 tttatatttg aaccttaaaa aattatttaa tcaaattcttt ttcactttaa aaacaaaata 180
 tccagaaaaa acaatagtta acggagggat aata atg aaa tac aag tca tca aaa 235
 Met Lys Tyr Lys Ser Ser Lys
 1 5
 gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act 283
 Val Ala Met Cys Thr Leu Ser Ala Leu Met Leu Ser Thr Ile Ala Thr
 10 15 20
 cca agt ata tct gtt ttc gct gca gaa aca act tcg tca cat gcg gtt 331
 Pro Ser Ile Ser Val Phe Ala Ala Glu Thr Thr Ser Ser His Ala Val
 25 30 35
 act aat cag caa aca att acg cag cgt gca gaa tct tat att gat att 379
 Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile
 40 45 50 55

38-21(52806) Sequence Listing_PCT_2.ST25.txt

gtg cac aat aga atg aaa caa aga gat att gaa tca aaa atg aca ggt Val His Asn Arg Met Lys Gln Arg Asp Ile Glu Ser Lys Met Thr Gly 60 65 70	427
aaa tcc att aat atg caa gaa caa ata att gat gga tgg ttt tta gct Lys Ser Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala 75 80 85	475
aga ttt tgg ata ttt aag gat caa aat aat agt cac caa aca aat aga Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Ser His Gln Thr Asn Arg 90 95 100	523
ttt att tca tgg ttt aag gat aat ttg gct agc cca gga ggg tat gat Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Pro Gly Gly Tyr Asp 105 110 115	571
agt atc gct gaa cag atg ggc cta aaa gta gca gca tta aat gat atg Ser Ile Ala Glu Gln Met Gly Leu Lys Val Ala Ala Leu Asn Asp Met 120 125 130 135	619
gat ata tca aat gta aat tat act tct aag aca ggg gat act ata tat Asp Ile Ser Asn Val Asn Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr 140 145 150	667
aat ggt gtt tca gaa tta aaa aat atc aca gga aca act caa aaa atg Asn Gly Val Ser Glu Leu Lys Asn Ile Thr Gly Thr Thr Gln Lys Met 155 160 165	715
aaa aca gat agt ttt caa aga gat tat aca aaa tcc cag tca act tca Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Gln Ser Thr Ser 170 175 180	763
atc acc aat gga tta caa tta gga ttt aaa gtt tca gct aaa gga ata Ile Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ser Ala Lys Gly Ile 185 190 195	811
gtg gcc tta gcc ggt gcg gat ttt gaa gca agt gta aac tat aat tta Val Ala Leu Ala Gly Ala Asp Phe Glu Ala Ser Val Asn Tyr Asn Leu 200 205 210 215	859
tcc act acc gca act gaa acc aat aca ata tct gat aaa ttt acc gtt Ser Thr Thr Ala Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val 220 225 230	907
cct tca caa gaa gtc aca tta gcg cca gga cat aag gcg atc gta aaa Pro Ser Gln Glu Val Thr Leu Ala Pro Gly His Lys Ala Ile Val Lys 235 240 245	955
cat agt ttg aag aaa atg gta tac tct gga acg cat gat tta aaa gga His Ser Leu Lys Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly 250 255 260	1003
gat tta aca att act ttt aat gat aag gat tta gtt caa aaa ttt att Asp Leu Thr Ile Thr Phe Asn Asp Lys Asp Leu Val Gln Lys Phe Ile 265 270 275	1051
tat cca aat tat aaa gct att gat tta tct aat att cgt aaa gca atg Tyr Pro Asn Tyr Lys Ala Ile Asp Leu Ser Asn Ile Arg Lys Ala Met 280 285 290 295	1099
aca gaa att gat gaa tgg aat cat gta aaa cct acc gat ttc tat caa Thr Glu Ile Asp Glu Trp Asn His Val Lys Pro Thr Asp Phe Tyr Gln	1147

38-21(52806) Sequence Listing_PCT_2.ST25.txt
 300 305 310

tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc 1195
 Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile 315 320 325

gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca 1243
 Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr 330 335 340

gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag 1291
 Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys 345 350 355

cgt tta aat aac aaa taagttactt aaaggtaatt cattaacaat gtatccatta 1346
 Arg Leu Asn Asn Lys 360

tataattaat ttataaaaat aatgttttaa aa 1378

<210> 10

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 10

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu
 1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
 20 25 30

Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp
 50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
 100 105 110

Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser
 130 135 140
 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile
 145 150 155 160
 Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175
 Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190
 Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205
 Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr
 210 215 220
 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro
 225 230 235 240
 Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser
 245 250 255
 Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys
 260 265 270
 Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu
 275 280 285
 Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val
 290 295 300
 Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys
 305 310 315 320
 Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn
 325 330 335
 Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn
 340 345 350
 Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys
 355 360

<210> 11.

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set forth in SEQ ID NO 3 from 438-458, biased toward codons preferred in Bacillus species genes containing A or T in 3rd position

 <400> 11
 aataataatc atcaaacwaa t 21

 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 978- 998, biased toward codons preferred in Bacillus species genes in which A or T is in 3rd position

 <400> 12
 attwggataw ataaattttt g 21

 <210> 13
 <211> 1101
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> coding sequence preferred for use in monocot species encoding a B t TIC901 amino acid sequence variant

 <220>
 <221> CDS
 <222> (1)..(1101)
 <223>

38-21(52806) Sequence Listing_PCT_2.ST25.txt

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<400> 13
atg aag aac cgc ttc agc aag gtc gcc ctc tgc acg gtg cct atc ctc      48
Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
1 5 10 15

atg gtt tct acg ttc gcg tcc agc tcg atg tcc gcg ttc gca gcg gag      96
Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
20 25 30

gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac      144
Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
35 40 45

gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac      192
Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
50 55 60

aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc      240
Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac      288
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat aac atc      336
Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
100 105 110

gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa      384
Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
115 120 125

atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt      432
Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
130 135 140

aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat      480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
145 150 155 160

acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac      528
Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175

aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc      576
Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag      624
Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca      672
Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
210 215 220

att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca      720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
225 230 235 240

```

38-21(52806) sequence Listing_PCT_2.ST25.txt

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ggc cac aag gca atc gtc aag cac gac ctg agg aaa atg gtc tac agc      768
Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
                245                250                255

ggc acc cat gat ctc aaa ggc gac ctc atc gtg tcg ttc aac gac aag      816
Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
                260                265                270

gag ata gtc cag aag ttc atc tac cca aat tac cgc gac atc aac ctc      864
Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
                275                280                285

agt gac atc cga gag acc atg atc gag atc gac gag tgg aac cac gtg      912
Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
                290                295                300

aac cct gtc aat ttc tac gaa ctc gta gga gtt aag aac cac atc aag      960
Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
                305                310                315                320

aac ggt gaa aca ttg tac atc gac acg ccg gct aag ttc atg ttc aac     1008
Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
                325                330                335

gga gcg aat cct tac tat cga gct acc ttc acg gag tac gat ggc aac     1056
Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
                340                345                350

aac aat cct gtt cag acc aag gtg ttg agt gag aat ttc aag ctg      1101
Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
                355                360                365

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<210> 14

<211> 367

<212> PRT

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a B
t TIC901 amino acid sequence variant

<400> 14

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Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
1          5          10          15

```

```

Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
                20          25          30

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```

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
35          40          45

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38-21(52806) Sequence Listing_PCT_2.ST25.txt

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
 50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
 100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
 145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
 225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
 275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
 290 295 300

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
 340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
 355 360 365

<210> 15

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in thermal amplification reactions

<400> 15

cctttggcag aaactttaac tcc

23

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in thermal amplification reactions

<400> 16

gtgtattctg gtacgcatga c

21

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<220>

<223> oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in thermal amplification reactions

<400> 17

gccgatccc tagctgaata tgcagtagat aatg

34

<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in thermal amplification reactions

<400> 18

gtggcacgtt tataggccat tgttc

25

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in thermal amplification reactions

<400> 19

cttttaggcc catctgttca gcg

23

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in thermal amplification reactions

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<400> 20
gccttagccg gtgcggattt tgaagc 26

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in thermal amplification reactions

<400> 21
ggagcttatt tggtatttaa acgctttggt ttgacttgat ttcc 44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in thermal amplification reactions

<400> 22
gccggatccc agtggatagg aatttgtttt cgtgctagg 39

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplification of from about 600 to about 650 base pairs

<400> 23
aayatgcarg arcarathat hgaygg 26

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24
 aayatgcarg arcarathat hga 23

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25
 aayatgcarg arcarathat 20

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> universal forward amplification primer that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<220>

<221> misc_feature

<222> (3)..(3)

<223> inosine

<220>

<221> misc_feature

<222> (9)..(9)

<223> inosine

<400> 26

ggngayacna thtayaaygg

20

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:28 and
SEQ ID NO:29

<220>

<221> misc_feature

<222> (6)..(6)

<223> inosine

<220>

<221> misc_feature

<222> (24)..(24)

<223> inosine

<400> 27

tarttnggrt adatraaytt ytnac

26

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<210> 28
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:29
 <220>
 <221> misc_feature
 <222> (6)..(6)
 <223> inosine

 <400> 28
 tarttnggrt adatraaytt ytg 23

 <210> 29
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:28
 <220>
 <221> misc_feature
 <222> (18)..(18)
 <223> inosine

 <400> 29
 ggrtadata aytttgnac 20

 <210> 30
 <211> 570
 <212> DNA

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(570)

<223>

<400> 30

ttt	tta	gct	aga	ttt	tgg	ata	ttt	gag	gat	caa	aat	aat	agt	cac	caa	48
Phe	Leu	Ala	Arg	Phe	Trp	Ile	Phe	Glu	Asp	Gln	Asn	Asn	Ser	His	Gln	
1				5				10						15		

aca	aat	aga	ttt	att	tca	tgg	ttt	aag	gat	aat	att	gct	agt	tca	aaa	96
Thr	Asn	Arg	Phe	Ile	Ser	Trp	Phe	Lys	Asp	Asn	Ile	Ala	Ser	Ser	Lys	
			20					25					30			

ggg	tat	aat	agt	att	gcg	gag	caa	atg	ggt	tta	aaa	ata	gaa	gca	gaa	144
Gly	Tyr	Asn	Ser	Ile	Ala	Glu	Gln	Met	Gly	Leu	Lys	Ile	Glu	Ala	Glu	
		35				40					45					

aac	gat	atg	gat	gta	aca	aat	ata	gat	tat	aca	tct	aag	aca	ggc	gat	192
Asn	Asp	Met	Asp	Val	Thr	Asn	Ile	Asp	Tyr	Thr	Ser	Lys	Thr	Gly	Asp	
	50					55					60					

acc	att	tat	aat	ggt	att	tca	gaa	ttg	aaa	aat	tat	aca	gga	tca	act	240
Thr	Ile	Tyr	Asn	Gly	Ile	Ser	Glu	Leu	Lys	Asn	Tyr	Thr	Gly	Ser	Thr	
65				70					75						80	

caa	aag	atg	aaa	aca	gat	agt	ttt	caa	aga	gat	tat	aca	aaa	tca	gaa	288
Gln	Lys	Met	Lys	Thr	Asp	Ser	Phe	Gln	Arg	Asp	Tyr	Thr	Lys	Ser	Glu	
				85				90						95		

tct	act	tca	gta	act	aat	gga	tta	caa	tta	gga	ttt	aaa	gtt	gct	gct	336
Ser	Thr	Ser	Val	Thr	Asn	Gly	Leu	Gln	Leu	Gly	Phe	Lys	Val	Ala	Ala	
			100					105					110			

aaa	gga	gta	gtt	gct	ttg	gct	ggg	gca	gac	ttt	gaa	acc	agt	gtt	act	384
Lys	Gly	Val	Val	Ala	Leu	Ala	Gly	Ala	Asp	Phe	Glu	Thr	Ser	Val	Thr	
		115					120					125				

tat	aat	cta	tca	act	act	aca	act	gaa	aca	aat	aca	ata	tca	gac	aag	432
Tyr	Asn	Leu	Ser	Thr	Thr	Thr	Thr	Glu	Thr	Asn	Thr	Ile	Ser	Asp	Lys	
	130					135					140					

ttt	act	gtc	cca	tct	caa	gaa	gtt	aca	ttg	cct	cca	gga	cat	aaa	gcg	480
Phe	Thr	Val	Pro	Ser	Gln	Glu	Val	Thr	Leu	Pro	Pro	Gly	His	Lys	Ala	
145					150					155					160	

ata	gtg	aaa	cat	gat	tta	aga	aaa	atg	gtt	tat	tct	ggt	act	cat	gat	528
Ile	Val	Lys	His	Asp	Leu	Arg	Lys	Met	Val	Tyr	Ser	Gly	Thr	His	Asp	
				165					170					175		

cta	aag	ggt	gat	tta	att	gtg	agt	ttt	aat	gat	aaa	gag	att			570
Leu	Lys	Gly	Asp	Leu	Ile	Val	Ser	Phe	Asn	Asp	Lys	Glu	Ile			
			180					185					190			

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<210> 31

<211> 190

<212> PRT

<213> Bacillus thuringiensis

<400> 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln
 1 5 10 15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys
 20 25 30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu
 35 40 45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp
 50 55 60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr
 65 70 75 80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu
 85 90 95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala
 100 105 110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr
 115 120 125

Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys
 130 135 140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala
 145 150 155 160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp
 165 170 175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile
 180 185 190

<210> 32

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<211> 1095

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)..(1092)

<223> sequence encoding TIC431 precursor amino acid sequence

<400> 32

atg	aaa	tac	aag	tct	tca	aaa	gta	gca	atg	tgt	aca	tta	tcg	gct	tta	48
Met	Lys	Tyr	Lys	Ser	Ser	Lys	Val	Ala	Met	Cys	Thr	Leu	Ser	Ala	Leu	
1				5				10						15		
atg	ctt	tcg	aca	atc	gcc	act	cca	agt	ata	tct	ggt	ttc	gct	gct	gaa	96
Met	Leu	Ser	Thr	Ile	Ala	Thr	Pro	Ser	Ile	Ser	Val	Phe	Ala	Ala	Glu	
			20					25					30			
aca	act	gca	tca	cat	aag	ggt	act	aat	cag	caa	aca	att	gca	cag	cgt	144
Thr	Thr	Ala	Ser	His	Lys	Val	Thr	Asn	Gln	Gln	Thr	Ile	Ala	Gln	Arg	
		35				40						45				
gca	gaa	tct	tat	atc	gat	att	gtg	cat	aat	aga	atg	aaa	aaa	cga	gat	192
Ala	Glu	Ser	Tyr	Ile	Asp	Ile	Val	His	Asn	Arg	Met	Lys	Lys	Arg	Asp	
	50					55					60					
att	gaa	tca	aaa	atg	aca	ggg	aaa	cct	att	aat	atg	caa	gaa	caa	ata	240
Ile	Glu	Ser	Lys	Met	Thr	Gly	Lys	Pro	Ile	Asn	Met	Gln	Glu	Gln	Ile	
65					70				75						80	
att	gat	gga	tgg	ttt	tta	gct	aga	ttt	tgg	ata	ttc	aag	gac	caa	aat	288
Ile	Asp	Gly	Trp	Phe	Leu	Ala	Arg	Phe	Trp	Ile	Phe	Lys	Asp	Gln	Asn	
				85				90						95		
aat	agt	cac	caa	aca	aat	aga	ttt	att	tca	tgg	ttt	aaa	gat	aat	tta	336
Asn	Ser	His	Gln	Thr	Asn	Arg	Phe	Ile	Ser	Trp	Phe	Lys	Asp	Asn	Leu	
			100					105					110			
gct	agt	cca	gga	ggg	tat	aat	agt	atc	gct	aaa	caa	atg	ggg	tta	aaa	384
Ala	Ser	Pro	Gly	Gly	Tyr	Asn	Ser	Ile	Ala	Lys	Gln	Met	Gly	Leu	Lys	
		115					120					125				
ata	gaa	gta	tta	aat	gat	atg	gat	ata	tca	aat	gta	aat	tat	act	tct	432
Ile	Glu	Val	Leu	Asn	Asp	Met	Asp	Ile	Ser	Asn	Val	Asn	Tyr	Thr	Ser	
	130					135					140					
aag	aca	ggg	gat	act	ata	tat	aat	ggg	ggt	tcc	gaa	tta	aaa	aat	atc	480
Lys	Thr	Gly	Asp	Thr	Ile	Tyr	Asn	Gly	Val	Ser	Glu	Leu	Lys	Asn	Ile	
145					150				155						160	
aca	ggg	aca	act	caa	aaa	atg	aaa	aca	gat	agt	ttt	caa	aga	gat	tat	528
Thr	Gly	Thr	Thr	Gln	Lys	Met	Lys	Thr	Asp	Ser	Phe	Gln	Arg	Asp	Tyr	
				165					170					175		

38-21(52806) Sequence Listing_PCT_2.ST25.txt

aca Thr	aaa Lys	tca Ser	cag Gln 180	tca Ser	act Thr	tca Ser	atc Ile 185	acc Thr 185	aat Asn	gga Gly	tta Leu	caa Gln 190	tta Leu 190	gga Gly	ttt Phe	576
aaa Lys	gtt Val	tct Ser 195	gcc Ala	aaa Lys	ggg Gly	gtg Val 200	ata Ile 200	gct Ala	tta Leu	gca Ala	gga Gly 205	gca Ala 205	gac Asp	ttc Phe	gaa Glu	624
gca Ala 210	agt Ser 210	gtc Val	aac Asn	tat Tyr	aat Asn 215	tta Leu 215	tcc Ser	act Thr	acc Thr	gca Ala	act Thr 220	gaa Glu	acc Thr	aat Asn	ata Ile	672
ata Ile 225	tct Ser	gat Asp	aaa Lys	ttt Phe	acc Thr 230	gtt Val	cct Pro	tca Ser	caa Gln	gaa Glu 235	gtt Val	aca Thr	tta Leu	gcg Ala	cca Pro 240	720
gga Gly	cat His	aag Lys	gcg Ala 245	atc Ile 245	gta Val	aaa Lys	cat His	agt Ser	tta Leu 250	aag Lys	aaa Lys	atg Met	gta Val	tac Tyr 255	tcc Ser	768
gga Gly	acg Thr	cat His	gat Asp 260	tta Leu	aaa Lys	gga Gly	gat Asp 265	tta Leu 265	aca Thr	att Ile	act Thr	ttt Phe	aat Asn 270	gat Asp	aag Lys	816
gat Asp	tta Leu	gtt Val 275	caa Gln	aaa Lys	ttt Phe	att Ile	tat Tyr 280	cca Pro	aat Asn	tat Tyr	aaa Lys	gct Ala 285	att Ile	gat Asp	tta Leu	864
tct Ser 290	aat Asn 290	att Ile	cgt Arg	aaa Lys	gca Ala	ctg Leu 295	act Thr	gaa Glu	att Ile	gat Asp	gaa Glu 300	tgg Trp	aat Asn	cat His	gta Val	912
aaa Lys 305	cct Pro	acc Thr	gat Asp	ttc Phe 310	tat Tyr 310	caa Gln	tta Leu	gtt Val	ggg Gly 315	aac Asn 315	aaa Lys	aat Asn	tat Tyr	ata Ile	aaa Lys 320	960
aac Asn	ggg Gly	gac Asp	act Thr	tta Leu 325	tac Tyr	atc Ile	gaa Glu	aca Thr	cct Pro 330	gct Ala	aaa Lys	ttc Phe	act Thr	ttg Leu 335	aat Asn	1008
gga Gly	gga Gly	aac Asn	cct Pro 340	tat Tyr	tat Tyr	aca Thr	gca Ala	acc Thr 345	ttt Phe	acg Thr	gaa Glu	tat Tyr	gat Asp 350	gaa Glu	agt Ser	1056
gga Gly	aat Asn	caa Gln 355	gtc Val	aaa Lys	aca Thr	aag Lys	cat His 360	tta Leu	agt Ser	gtc Val	aaa Lys	taa				1095

<210> 33

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu

38-21(52806) Sequence Listing_PCT_2.ST25.txt

1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
20 25 30

Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp
50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
100 105 110

Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys
115 120 125

Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile
145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser
245 250 255

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu
275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser
340 345 350

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys
355 360